

## SUMMARIES

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/organism="Homo sapiens"  
/db_xref="taxon:9606"
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QY 601 aaagcctatactgaagccttaagaaagaatctgtccaccataccaccaagt 660  
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Db 1036 AAGCCATATGTGAAGACCTTAAGAAGAAAGAAATCTTCCACCTTACCACCAAGTG 1095  
QY 661 tctttaagcctcaacttga 681  
|||||  
Db 1096 TCTTTTACCTTCAACTTTGA 1116

RESULT 3  
HSA308569 4860 bp mRNA PRI 06-JUN-2001  
LOCUS Homo sapiens mRNA for leucine-rich repeat-containing 2 protein  
DEFINITION (LRRC2 gene).  
ACCESSION AJ308569.2 GI:14330408  
VERSION AJ308569.2 GI:14330408  
KEYWORDS leucine-rich repeat-containing 2 protein; LRRC2 gene.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 4860)  
AUTHORS Kiss, H., Yang, Y., Kost-Alimova, M., Szeles, A., Kholodnyuk, I.,  
Kedra, D., Kiss, C., Klein, G., Imreh, S. and Dumanaki, J.P.  
TITLE Transcriptional map of the Common Eliminated Region 1 on human  
3p21.3  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 4860)  
AUTHORS Kiss, H.  
TITLE Direct Submission  
JOURNAL Submitted (27-FEB-2001) Kiss H., Microbiology and Tumorbiology  
Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177,  
SWEDEN

REMARK Revised by [3]  
REFERENCE 3 (bases 1 to 4860)  
AUTHORS Kiss, H.  
TITLE Direct Submission  
JOURNAL Submitted (06-JUN-2001) Kiss H., Microbiology and Tumorbiology  
Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177,  
SWEDEN

COMMENT On Jun 8, 2001 this sequence version replaced gi:1318611.  
FEATURES  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="3"  
/map="3p21.3"  
168..1283  
/gene="LRRC2"  
168..1283  
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/codon\_start=1  
/product="leucine-rich repeat-containing 2 protein"  
/protein\_id="CAC33442.1"  
/db\_xref="GI:13186112"  
/translation="MGKVVVFDISVIRALMTRVKKHKKMOKEVERLEKSALEKIK  
EENMFALDRCRGIPOAYCKNGFIDTSVLDIKIRNTTROSSLPKDGKSSAFV  
FELSGHWTLEPDLSEKQTHLRMYISNTLIOTITPTIQLFQMRILDPKNSHIP  
AETGLKLNKELWGNFNLYKSTIPPELGDCEHLRDLCSGLEMELPEFLSNKOYTF  
VLSANKFSSVPCVLRMSNLQWLDISNNLTDLDPDIDLELELQSLYKNTLYLP  
YSMLNKKTLIVVSGDHLVEPLTALCDSTPLKPFVSLMDNPIDNAQCEDEGNEIMSE  
RDRQHEDEKVMKYEIDLEKRESVPYTTKVSFLQ"

BASE COUNT 1480 a 924 c 1162 g 1294 t  
ORIGIN

Query Match 100.0%; Score 681; DB 9; Length 4860;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgagaattctgagctgcacaaacacaaatctcacatctccagagaatcggtgt 60  
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Db 603 ATGAGAAATTCGTGATCTGCCAAAAAACCAATCTCACATCTTCAGCAGAAATCGGTTGT 662  
QY 61 ttgaagaaacctgaagaacctaatctggttcaactatactgaagagatctccacaa 120  
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Db 663 TTGAAGAACCTGAAAGAACTCAATGTGGTTTCAACTATCTGAAGAGCATTCCTCCAGAA 722  
QY 121 ttggagaatttgaaatctagaagagactgattgttctggaatctgaatgaatgag 180  
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Db 723 TTGGAGAGTTGTGAAATCTAGAGAGACTGATTTGTTCTGGAATCTGAAATTAATGAG 782  
QY 181 ctgccttgaatgaatgaatctgaagcaagttacatttgatagatctcagaacaag 240  
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Db 783 CTGCCCTTGAATTAAGAAATTTGAAGCAAGTTACATTTGATGATCTCAGCAAAAG 842  
QY 241 ttccagagtcaccaactgctgctcgtgagtgatgcgaattgtgagtgatgatacgc 300  
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Db 843 TTTTCCAGTGTCCCAATCTGTCTCTGGAGTGTGAAATTTGCAATGTTGATATTCAGC 902  
QY 301 agcaataacctgacacactgcgcgaagataagacagctagagagctgacagactt 360  
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Db 903 AGCAATAACCTGACCGACGACCTCCGCAAGATATGACAGCGCTAGAGAGCTCAGAGCTTT 962  
QY 361 ctcttgataaaacaagttgacctacctccattccatgctgacactgaagaagctc 420  
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Db 963 CTCTTGATATAAAACAAGTTGACCTACCTTCCATTCCATGCAAGCACTGAAGAAGCTC 1022  
QY 421 actctgttagctgcagtgaggagacattgtgtgagctcccaactgacctgtgaccca 480  
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Db 1023 ACTCTGTAGTGTGACAGGGGACCATTTGGTGAAGCTCCCAAGCTCCCTTTGTGACCA 1082  
QY 481 tccacaccttaaaatctgtaagccttaagacaatccattgataatgccaatgttaa 540  
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Db 1083 TCCACACCTTAAATTTGTAAGCTTATGACAACTCTATTGATGAATGCCCAATGTGAA 1142  
QY 541 gatggcaatgaataatgaaagtgaacggagatgcgaacatttgataaagaagtac 600  
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Db 1143 GATGGCAATGAATAATGGAAGAAAGTGAACGGATGCCCAACTTTTGATGAAGAAGTATG 1202  
QY 601 aaagcctatactgaagccttaagaaagaatctgtccaccataccaccaagt 660  
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Db 1203 AAGCCATATGTGAAGACCTTAAGAAGAAAGAAATCTTCCACCTTATACCAACCAAGTG 1262  
QY 661 tctttaagcctcaacttga 681  
|||||  
Db 1263 TCTTTTACCTTCAACTTTGA 1283

RESULT 4  
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LOCUS HSA310996 145795 bp DNA HTG 18-APR-2001  
DEFINITION Homo sapiens chromosome 3 clone RP6-91P17 map 3p21.3. \*\*\*  
SEQUENCING IN PROGRESS \*\*\*, 42 ordered pieces.  
ACCESSION AJ310996  
VERSION AJ310996.1 GI:13751170  
KEYWORDS HTG; HTGS\_PHASE2.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 145795)  
AUTHORS Kiss, H., Yang, Y., Kost-Alimova, M., Szeles, A., Kholodnyuk, I.,  
Kedra, D., Kiss, C., Klein, G., Imreh, S. and Dumanaki, J.P.  
TITLE Transcriptional map of the common eliminated region 1 on human  
3p21.3  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 145795)  
AUTHORS Kiss, H.  
TITLE Direct Submission  
JOURNAL Submitted (17-APR-2001) Kiss H., Microbiology and Tumorbiology  
Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177,  
SWEDEN

COMMENT The sequencing contigs are in order and the gaps between them are  
represented by 100 n's.

Contig 1: 1-2508 Contig 2: 2609-17434 Contig 3: 17535-21987  
Contig 4: 22088-23066 Contig 5: 23167-28845 Contig 8:  
Contig 6: 28946-30840 Contig 7: 30941-37879  
Contig 9: 39029-40834 Contig 10: 40935-44527 Contig  
11: 44628-48077 Contig 12: 48178-52755 Contig 13: 52856-53933  
Contig 14: 53394-54768 Contig 15: 54869-57895 Contig 16:  
57996-59922 Contig 17: 59423-60159 Contig 18: 60260-61231  
Contig 19: 61332-62928 Contig 20: 63029-63852 Contig 21:  
63953-75555 Contig 22: 75656-77760 Contig 23: 77861-79686  
Contig 24: 79787-80857 Contig 25: 80958-87622 Contig 26:  
87723-89164 Contig 27: 89265-90007 Contig 28: 90108-92035  
Contig 29: 92136-97298 Contig 30: 97399-102032 Contig 31:  
102133-106605 Contig 32: 106706-108263 Contig 33: 108364-110022  
Contig 34: 110123-113747 Contig 35: 113848-125151 Contig 36:  
125252-126026 Contig 37: 126127-129649 Contig 38: 129750-132160  
Contig 39: 132261-133125 Contig 40: 133226-135661 Contig 41:  
135763-142148 Contig 42: 142249-145795.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 42 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submittor.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
\* 1 2508: contig of 2508 bp in length  
\* 2509 2608: gap of 100 bp  
\* 2609 17434: contig of 14826 bp in length  
\* 17435 17534: gap of 100 bp  
\* 17535 21987: contig of 4453 bp in length  
\* 21988 22087: gap of 100 bp  
\* 22088 23066: contig of 979 bp in length  
\* 23067 23166: gap of 100 bp  
\* 23167 28845: contig of 5679 bp in length  
\* 28846 28945: gap of 100 bp  
\* 28946 30840: contig of 1895 bp in length  
\* 30841 30940: gap of 100 bp  
\* 30941 37879: contig of 6939 bp in length  
\* 37880 37979: gap of 100 bp  
\* 37980 38928: contig of 949 bp in length  
\* 38929 39028: gap of 100 bp  
\* 39029 40834: contig of 1806 bp in length  
\* 40835 40934: gap of 100 bp  
\* 40935 44527: contig of 3593 bp in length  
\* 44528 44627: gap of 100 bp  
\* 44628 48077: contig of 3450 bp in length  
\* 48078 48177: gap of 100 bp  
\* 48178 52755: contig of 4578 bp in length  
\* 52756 52855: gap of 100 bp  
\* 52856 53293: contig of 438 bp in length  
\* 53294 53393: gap of 100 bp  
\* 53394 54768: contig of 1375 bp in length  
\* 54769 54868: gap of 100 bp  
\* 54869 57895: contig of 3027 bp in length  
\* 57896 57995: gap of 100 bp  
\* 57996 59322: contig of 1327 bp in length  
\* 59323 59422: gap of 100 bp  
\* 59423 60159: contig of 737 bp in length  
\* 60160 60259: gap of 100 bp  
\* 60260 61231: contig of 972 bp in length  
\* 61232 61331: gap of 100 bp  
\* 61332 62928: contig of 1597 bp in length  
\* 62929 63028: gap of 100 bp  
\* 63029 63852: contig of 824 bp in length  
\* 63853 63952: gap of 100 bp  
\* 63953 75555: contig of 11603 bp in length  
\* 75556 75655: gap of 100 bp  
\* 75656 77760: contig of 2105 bp in length  
\* 77761 77860: gap of 100 bp  
\* 77861 79686: contig of 1826 bp in length  
\* 79687 79786: gap of 100 bp  
\* 79787 80857: contig of 1071 bp in length

\* 80858 80957: gap of 100 bp  
\* 80958 87622: contig of 6665 bp in length  
\* 87623 87722: gap of 100 bp  
\* 87723 89164: contig of 1442 bp in length  
\* 89165 89264: gap of 100 bp  
\* 89265 90007: contig of 743 bp in length  
\* 90008 90107: gap of 100 bp  
\* 90108 92035: contig of 1928 bp in length  
\* 92036 92135: gap of 100 bp  
\* 92136 97298: contig of 5163 bp in length  
\* 97299 97398: gap of 100 bp  
\* 97399 102032: contig of 4634 bp in length  
\* 102033 102132: gap of 100 bp  
\* 102133 106605: contig of 4473 bp in length  
\* 106606 106705: gap of 100 bp  
\* 106706 108263: contig of 1558 bp in length  
\* 108264 108363: gap of 100 bp  
\* 108364 110022: contig of 1659 bp in length  
\* 110023 110122: gap of 100 bp  
\* 110123 113747: contig of 3625 bp in length  
\* 113748 113847: gap of 100 bp  
\* 113848 125151: contig of 11304 bp in length  
\* 125152 125251: gap of 100 bp  
\* 125252 126026: contig of 775 bp in length  
\* 126027 126126: gap of 100 bp  
\* 126127 129649: contig of 3523 bp in length  
\* 129650 129749: gap of 100 bp  
\* 129750 132160: contig of 2411 bp in length  
\* 132161 132260: gap of 100 bp  
\* 132261 133125: contig of 865 bp in length  
\* 133126 133225: gap of 100 bp  
\* 133226 135661: contig of 2436 bp in length  
\* 135662 135761: gap of 100 bp  
\* 135762 142148: contig of 6387 bp in length  
\* 142149 142248: gap of 100 bp  
\* 142249 145795: contig of 3547 bp in length.

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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="3"  
/map="3p21.3"  
/clone="Rp6-91p17"

BASE COUNT 39764 a 33207 c 31499 g 37225 t 4100 others  
ORIGIN

Query Match 23.2% Score 158: DB 2: Length 145795;  
Best Local Similarity 100.0%; Pred. No. 2e-76;  
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 337 agcctagagagctgcgaagcttctctgtataaacaagttgacctaccctccat 396  
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DB 61617 AGGCTAAGAGAGCTGCAGAGCTTCTCTGTATAAAAACAAGTTACCTCCAT 61558  
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OY 397 tccatgctgaactgaagaagctcaactctgttagtcgtcagtgaggaccattggtgag 456  
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DB 61557 TCCATGCTGAACCTGAAGAAGCTCCTGTAGTCGTCAGGAGGACCATTTGGTGAG 61498  
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OY 457 ctcccaactgccccttggatgcattccacaccttaaa 494  
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DB 61497 CTCGCCACTGCCCTTTGTGACTATCATCACACCTTTAA 61460  
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RESULT 5  
AC068720 AC068720 202324 bp DNA HTG 07-JUL-2000  
LOCUS Homo sapiens chromosome 3 clone RP11-509121, WORKING DRAFT  
DEFINITION  
SEQUENCE, 20 unordered pieces.  
AC068720 AC068720 2 GI:8469022  
VERSION AC068720.2 GI:8469022  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE human.





BASE COUNT	642 a	394 c	495 g	525 t	
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Query Match	18.9%: Score 129; DB 9; Length 2056;				
Best Local Similarity	100.0%: Pred. No. 2,5e-60;				
Matches 129; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
Qy	553	ataatggaagtgaacgggacgcgaacatttgataaagaagtatgaagcctatat	612		
Db	1294	ATAATGGAAGTGAACGGGATCGCCAACATTTTGATATAAGAAGTTATGAAGCCTATATT	1353		
Qy	613	gaagacctaaagaagaaggaatcgtgtccacgcctataccaccagaagtgctttaagcctt	672		
Db	1354	GAAAGACCTTAAAGAAGAAGATCGTGTCCAGCTATACACCAAGAAGTGCTTTTACGCTT	1413		
Qy	673	caacttga 681			
Db	1414	CAACTTGA 1422			
RESULT 8					
AC013467/c					
LOCUS	AC013467	172966 bp	DNA	PRI	25-MAY-2001
DEFINITION	Homo sapiens clone RP11-451F14, complete sequence.				
ACCESSION	AC013467				
VERSION	AC013467.8	GI:14196420			
KEYWORDS	HTG.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE					
AUTHORS	1 (bases 1 to 172966)				
TITLE	Waterston,R.H.				
JOURNAL	The sequence of Homo sapiens clone				
AUTHORS	2 (bases 1 to 172966)				
TITLE	Waterston,R.H.				
JOURNAL	Direct Submission				
AUTHORS	Submitted (12-NOV-1999) Genome Sequencing Center, Washington				
TITLE	University School of Medicine, 4444 Forest Park Parkway, St. Louis,				
JOURNAL	MO 63108, USA				
REFERENCE	3 (bases 1 to 172966)				
AUTHORS	Waterston,R.H.				
TITLE	Direct Submission				
JOURNAL	Submitted (25-MAY-2001) Genome Sequencing Center, Washington				
AUTHORS	University School of Medicine, 4444 Forest Park Parkway, St. Louis,				
TITLE	MO 63108, USA				
JOURNAL	On May 25, 2001 this sequence version replaced gi:13624417.				
COMMENT	Center project name: H.NH0451F14.				
FEATURES	Location/Qualifiers				
SOURCE	1..172966				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/clone="RP11-451F14"				
BASE COUNT	57371 a	34327 c	31782 g	49486 t	
ORIGIN					
Query Match	5.3%: Score 36; DB 9; Length 172966;				
Best Local Similarity	100.0%: Pred. No. 1.8e-08;				
Matches 36; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
Qy	220	gtagatatctcagcaacaagtttcacagtgatcca	255		
Db	168708	GTAGATATCTCAGCAACAAGTTTTCACAGTGATCCA	168673		

RESULT 9  
AC025574 155929 bp DNA HTG 06-SEP-2000  
LOCUS Homo sapiens chromosome 12 clone RP11-348M3, WORKING DRAFT  
DEFINITION SQUENCE, 14 unordered pieces.  
AC025574  
VERSION AC025574.10 GI:9438393  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 155929)  
AUTHORS Muzny,D.M., Adams,C., Bailey,M., Barbara,J., Blankenburg,K., Bodota,B., Boucek,J., Bowie,S., Brooks,A., Buhay,C., Bunac,C., Burdett,C., Burrows,J., Carter,M., Chacko,J., Chen,Z., Cox,C., Dugan,R., Delgado,O., Deshazo,D., Ding,Y., Domah-Rashid,N., Forcum-Tansey,J., Frantz,P., Ganesha,R., Gorrell,J.H., Gorrell,L.L., Guvera,M., Harris,K., Hernandez,J., Hodgson,A., Hogues,M., Hollway,C., Hosak,H., Jackson,L.E., Jackson,L., Jia,Y., Jones,M., Kelly,S., Kondolewski,N., Kong,Y., Kovar,C., Leal,B., Li,Z., Licharge,O., Liu,J., Liu,M., Logan,O., Lozano,R.J., Lu,J., Lucier,R., Martin,R., Martinez,C., McLeod,M.P., Mel,G., Morgan,M., Morris,S., Nash,S., Nelson,A., Nguyen,R., Nguyen,N., Nguyen,S., Owsal,G., Parish,B., Paxton,S., Payton,B., Perez,L., Pu,L.L., Quiles,M., Reiter,D., Rives,M., Samuel,S., Say,J., Scherer,S., Shah,E., Shen,H., Simon,M., Sparks,A., Stamps,A., Sucgang,R., Taber,P., Taylor,T., Vasquez,L., Vinson,R., Vo,Q., Wahbah,M., Watlington,S., Weinstein,G., Weinstein,I.R., Williamson,A., Worley,K., Wren,J., Wrensford,G., Yu,W., Zhou,X., Nelson,D. and Gibbs,R.  
Direct Submission  
Unpublished  
2 (bases 1 to 155929)  
Worley,K.C.  
Direct Submission  
Submitted (11-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Jul 25, 2000 this sequence version replaced gi:8571540.  
COMMENT  
----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: HAIT  
Center Clone name: RP11-348M3  
----- Summary Statistics  
Sequencing vector: M13; L08821  
Chemistry: Dye-terminator Big Dye; 94% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 133622 bases at least Q40  
Consensus quality: 145733 bases at least Q30  
Consensus quality: 150334 bases at least Q20  
Estimated insert size: 150694; sum-of-ctnigs estimation  
Quality coverage: 0x in Q20 bases; agrose-fp estimation  
Quality coverage: 3.9x in Q20 bases; sum-of-ctnigs estimation  
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\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 14 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1 36972: contig of 36972 bp in length

FEATURES  
source 1..155929  
/organism="Homo sapiens"  
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/chromosome="12"  
/clone="RP11-348M3"  
Location/Qualifiers  
1..155929  
BASE COUNT 40876 a 36387 c 36205 g 41119 t 1342 others  
ORIGIN  
Query Match 3.2%; Score 22; DB 2; Length 155929;  
Best Local Similarity 100.0%; Pred.No. 1,1;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 464 ctgcccttgactcacc 485  
|||||  
Db 154274 CTGCCCTTGACTCACC 154295  
RESULT 10  
AC090521 77644 bp DNA INV 27-FEB-2001  
LOCUS Caenorhabditis briggsae cosmid CB002D19, complete sequence.  
DEFINITION AC090521  
AC090521  
VERSION AC090521.1 GI:13129524  
KEYWORDS HTG.  
SOURCE Caenorhabditis briggsae.  
ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Rhabditidae; Peleiderinae; Caenorhabditis.  
REFERENCE 1 (bases 1 to 77644)  
AUTHORS Washington University Genome Sequencing Center.  
TITLE The C. briggsae Genome Sequencing Project  
JOURNAL Unpublished  
2 (bases 1 to 77644)  
REFERENCE  
AUTHORS Waterston,R.  
TITLE Direct Submission  
JOURNAL Submitted (27-FEB-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
COMMENT  
Genome Sequencing Center  
Department of Genetics, Washington University,  
St. Louis, MO 63110, USA  
e-mail: jspethewatson.wustl.edu

NOTICE: This sequence may not be the entire insert of this clone.



It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

FEATURES  
source  
Location/Qualifiers  
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/organism="Caenorhabditis briggsae"  
/strain="Gujarat G16"  
/db\_xref="taxon:6238"  
/clone="CB002D19"  
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/note="codon recognized: AAA"  
/product="tRNA-Lys"  
BASE COUNT 22191 a 14948 c 15587 g 24918 t  
ORIGIN

Query Match 3.1%; Score 21; DB 3; Length 77644;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 ctgccaaaacccaatctca 36  
|||||  
Db 62656 CTGCCAAAACCAATCTCA 62676

RESULT 11  
LOCUS AC011381 109549 bp DNA HTG 23-APR-2001  
DEFINITION Homo sapiens chromosome 5 clone CTB-133N3, WORKING DRAFT SEQUENCE,  
7 unordered pieces.  
ACCESSION AC011381  
VERSION AC011381.5 GI:8576058  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ACTIVEFIN.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE 1 (bases 1 to 109549)  
JOURNAL DOE Joint Genome Institute.  
REFERENCE  
AUTHORS Sequencing of Human Chromosome 5  
TITLE 2 (bases 1 to 109549)  
JOURNAL DOE Joint Genome Institute.  
REFERENCE  
AUTHORS Direct Submission  
TITLE Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint  
JOURNAL Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
COMMENT On Jun 21, 2000 this sequence version replaced gi:7710349.  
-----Genome Center  
Center: Joint Genome Institute  
Center Code: JGI  
Web site: http://www.jgi.doe.gov.

Project Information  
Center Project Name: 115591, H239  
Center clone name: CIT978SKB\_133N3

Summary Statistics  
Consensus quality: 98174 bases at least Q40  
Consensus quality: 103469 bases at least Q30  
Consensus quality: 105214 bases at least Q20  
Estimated insert size: 110000; pulse field gel estimation  
Estimated insert size: 108949; sum-of-ctdigs estimation  
Quality coverage: 5.98 in Q20 bases; pulse field gel estimation  
Quality coverage: 6.04 in Q20 bases; sum-of-ctdigs estimation  
NOTE: This is a 'working draft' sequence. It currently  
\* consists of 7 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1 1231: contig of 1231 bp in length

\* 1232 1331: gap of unknown length  
\* 1332 8134: contig of 6803 bp in length  
\* 8135 8234: gap of unknown length  
\* 8235 15598: contig of 7364 bp in length  
\* 15599 15698: gap of unknown length  
\* 15699 22852: contig of 7154 bp in length  
\* 22853 22952: gap of unknown length  
\* 22953 30470: contig of 7518 bp in length  
\* 30471 30570: gap of unknown length  
\* 30571 59501: contig of 28931 bp in length  
\* 59502 59601: gap of unknown length  
\* 59602 109549: contig of 49948 bp in length.  
location/Qualifiers  
1..109549  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="5"  
/clone="CTB-133N3"  
/clone\_lib="Caltech human BAC library B"  
BASE COUNT 31123 a 25360 c 23787 g 28626 t 653 others  
ORIGIN

Query Match 3.1%; Score 21; DB 2; Length 109549;  
Best Local Similarity 100.0%; Pred. No. 4;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 578 aacatttgataagaagta 598  
|||||  
Db 109083 AACATTGTGATPAAAGAGTTA 109103

RESULT 12  
LOCUS AC004821 163332 bp DNA PRI 16-NOV-2000  
DEFINITION Homo sapiens clone RPI-98022, complete sequence.  
ACCESSION AC004821  
VERSION AC004821.3 GI:11181836  
KEYWORDS HTG.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE 1 (bases 1 to 163332)  
JOURNAL Waterston, R.H.  
REFERENCE  
AUTHORS The sequence of Homo sapiens clone  
TITLE 2 (bases 1 to 163332)  
JOURNAL Waterston, R.H.  
REFERENCE  
AUTHORS Direct Submission  
TITLE Submitted (12-JUN-1998) Genome Sequencing Center, Washington  
JOURNAL University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
REFERENCE  
AUTHORS 3 (bases 1 to 163332)  
JOURNAL Waterston, R.H.  
REFERENCE  
AUTHORS Direct Submission  
TITLE Submitted (05-MAY-1999) Genome Sequencing Center, Washington  
JOURNAL University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA

Project Information  
Center Project Name: 115591, H239  
Center clone name: CIT978SKB\_133N3

Summary Statistics  
Consensus quality: 98174 bases at least Q40  
Consensus quality: 103469 bases at least Q30  
Consensus quality: 105214 bases at least Q20  
Estimated insert size: 110000; pulse field gel estimation  
Estimated insert size: 108949; sum-of-ctdigs estimation  
Quality coverage: 5.98 in Q20 bases; pulse field gel estimation  
Quality coverage: 6.04 in Q20 bases; sum-of-ctdigs estimation  
NOTE: This is a 'working draft' sequence. It currently  
\* consists of 7 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1 1231: contig of 1231 bp in length

```

source          1. 163332
                /Organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="RP1-98022"
BASE COUNT      44502 a 38204 c 37986 g 42640 t
ORIGIN
Query Match     3.1%; Score 21; DB 9; Length 163332;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 578 aacatttgataagaagatga 598
      |||||
Db 4554 AACATTTCATTAAGAGAGTTA 4534

RESULT 13
AC016521 180541 bp DNA HTG 13-DEC-2000
LOCUS Homo sapiens clone RP11-29F8, WORKING DRAFT SEQUENCE, 17 unordered
DEFINITION
ACCESSION AC016521
VERSION AC016521.4 GI:11693419
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 180541)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens, clone RP11-29F8
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 180541)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collamore,A.,
Cooke,P., Dearellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heathford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehocky,J., Lieu,C., Locke,K., MacDonald,P., Margulis,N.,
McGowan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Teefaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
DIRECT SUBMISSION
Submitted (01-DEC-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Dec 13, 2000 this sequence version replaced gi:11693419.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L4829
Center clone name: 29_F_8
----- Summary Statistics
Sequencing vector: M13; M7815; 3% of reads
Chemistry: Dye-terminator Big Dye, 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 174572 bases at least Q40
Consensus quality: 177046 bases at least Q30
Consensus quality: 178064 bases at least Q20
Insert size: 16400; agarose-fp
Insert size: 178941; sum-of-ctrls

```

```

Quality coverage: 6.9 in Q20 bases; agarose-fp
Quality coverage: 7.1 in Q20 base.
NOTE: This is a 'working draft' sequence. It currently
consists of 17 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
1
863 962: gap of 100 bp
963 1717: contig of 755 bp in length
1718 1817: gap of 100 bp
1818 3133: contig of 1316 bp in length
3134 3233: gap of 100 bp
3234 4640: contig of 1407 bp in length
4641 4740: gap of 100 bp
4741 8634: contig of 3894 bp in length
8635 8734: gap of 100 bp
8735 10546: contig of 1812 bp in length
10547 10646: gap of 100 bp
10647 13769: contig of 3123 bp in length
13770 13869: gap of 100 bp
13870 17470: contig of 3601 bp in length
17471 17570: gap of 100 bp
17571 22684: contig of 5114 bp in length
22685 22784: gap of 100 bp
22785 31278: contig of 8494 bp in length
31279 31378: gap of 100 bp
31379 43626: contig of 12248 bp in length
43627 43726: gap of 100 bp
43727 56284: contig of 12558 bp in length
56285 56384: gap of 100 bp
56385 66809: contig of 10425 bp in length
66810 66909: gap of 100 bp
66910 86271: contig of 19362 bp in length
86272 86371: gap of 100 bp
86372 103947: contig of 17576 bp in length
103948 104047: gap of 100 bp
104048 137483: contig of 33436 bp in length
137484 137583: gap of 100 bp
137584 180541: contig of 42958 bp in length.
Location/Qualifiers
1. 180541
/Organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-29F8"
/clone_lib="RP11-11 Human Male BAC"
1. 862
/note="assembly_fragment
clone_end:SP6
vector_side:left"
963. 1717
/note="assembly_fragment"
1818. 3133
/note="assembly_fragment"
3234. 4640
/note="assembly_fragment"
4741. 8634
/note="assembly_fragment"
8735. 10546
/note="assembly_fragment"
10647. 13769
/note="assembly_fragment"
13870. 17470
/note="assembly_fragment"
17571. 22684
/note="assembly_fragment"
22785. 31278
/note="assembly_fragment"
31379. 43626
/note="assembly_fragment"

```

```
vector_side:right"
BASE COUNT      50954 a 38430 c 39265 g 50267 t 1625 others
ORIGIN
```

```

Query Match      3.1%; Score 21; DB 2; Length 180541;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
QY      338  ggctagagagctgcagagct 358
          |||||
Db 49823 GGCTAGAGGAGCTGCAGAGCT 49843
```

RESULT	14
AC022182	
LOCUS	AC022182 19379 bp DNA HTG 03-MAR-2000
DEFINITION	Homo sapiens chromosome 8 clone RP11-174G1 map 8, *** SEQUENCING IN
PROGESS	*** 71 unordered pieces.
ACCESSION	AC022182
VERSION	AC022182.3 GI:7143437
KEYWORDS	HTG; HTGS_PPHASE1.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE
1 (phases 1 to 193379)	Bliren,B., Linton,L., Nusbaum,C. and Lander,E.	Homo sapiens chromosome 8, clone RP11-174G1		
2 (phases 1 to 193379)	Bliren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,			

TITLE	Direct Submission
JOURNAL	Submitted (26-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, MA 02141, USA
COMMENT	On Mar 2, 2000 this sequence version replaced gi:6778580.

Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

```
----- Project Information
Center project name: L2078
Center clone name: 174_G_1
```

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 71 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1	1101: contig of 1101 bp in length
1102	1201: gap of 100 bp
1202	2413: contig of 1212 bp in length
2414	2513: gap of 100 bp
2514	3659: contig of 1146 bp in length
3660	3759: gap of 100 bp
3760	4954: contig of 1195 bp in length
4955	5054: gap of 100 bp
5055	6263: contig of 1209 bp in length
6264	6563: gap of 100 bp
6564	7674: contig of 1311 bp in length
7675	7774: gap of 100 bp
7775	8947: contig of 1173 bp in length
8948	9047: gap of 100 bp
9048	10331: contig of 1284 bp in length
10332	10431: gap of 100 bp
10432	11560: contig of 1129 bp in length
11561	11660: gap of 100 bp
11661	13003: contig of 1343 bp in length
13004	13103: gap of 100 bp
13104	14280: contig of 1177 bp in length
14281	14380: gap of 100 bp
14381	15516: contig of 1136 bp in length
15517	16166: gap of 100 bp
16167	16628: contig of 1212 bp in length
16629	16928: gap of 100 bp
16929	18200: contig of 1272 bp in length
18201	18300: gap of 100 bp
18301	18991: contig of 1691 bp in length
18992	20091: gap of 100 bp
20092	21666: contig of 1575 bp in length
21667	21766: gap of 100 bp
21767	21990: contig of 224 bp in length
21991	22090: gap of 100 bp
22091	23799: contig of 1709 bp in length
23800	23899: gap of 100 bp
23900	25582: contig of 1483 bp in length
25583	25482: gap of 100 bp
25483	27017: contig of 1535 bp in length
27018	27117: gap of 100 bp
27118	28348: contig of 1231 bp in length
28349	28448: gap of 100 bp
28449	29904: contig of 1456 bp in length
29905	30004: gap of 100 bp
30005	31690: contig of 1686 bp in length
31691	31790: gap of 100 bp
31791	32911: contig of 1121 bp in length
32912	33011: gap of 100 bp
33012	34436: contig of 1425 bp in length
34437	34536: gap of 100 bp
34537	35645: contig of 1309 bp in length
35646	35945: gap of 100 bp
35946	37171: contig of 1226 bp in length
37172	37271: gap of 100 bp
37272	38676: contig of 1296 bp in length
38678	38667: gap of 100 bp
38668	40850: contig of 2183 bp in length
40881	40950: gap of 100 bp
40951	42734: contig of 1784 bp in length
42735	42834: gap of 100 bp
42835	44226: contig of 1392 bp in length

```

* 44227 44326: gap of 100 bp
* 44327 45918: contig of 1592 bp in length
* 45919 46018: gap of 100 bp
* 46019 47637: contig of 1619 bp in length
* 47638 47737: gap of 100 bp
* 47738 49872: contig of 2135 bp in length
* 49873 49972: gap of 100 bp
* 49973 52711: contig of 2739 bp in length
* 52712 52811: gap of 100 bp
* 52812 55253: contig of 2442 bp in length
* 55254 55353: gap of 100 bp
* 55354 56537: contig of 1184 bp in length
* 56538 56637: gap of 100 bp
* 56638 58784: contig of 2147 bp in length
* 58785 58884: gap of 100 bp
* 58885 61009: contig of 2125 bp in length
* 61010 61109: gap of 100 bp
* 61110 63658: contig of 2549 bp in length
* 63659 63758: gap of 100 bp
* 63759 64988: contig of 1230 bp in length
* 64989 65088: gap of 100 bp
* 65089 66555: contig of 1467 bp in length
* 66556 66655: gap of 100 bp
* 66656 69110: contig of 2455 bp in length
* 69111 69210: gap of 100 bp
* 69211 71149: contig of 1939 bp in length
* 71150 71249: gap of 100 bp
* 71250 73237: contig of 1988 bp in length
* 73238 73337: gap of 100 bp
* 73338 76363: contig of 3026 bp in length
* 76364 76463: gap of 100 bp
* 76464 78717: contig of 2254 bp in length
* 78718 78817: gap of 100 bp
* 78818 81222: contig of 2405 bp in length
* 81223 81322: gap of 100 bp
* 81323 84081: contig of 2759 bp in length
* 84082 84181: gap of 100 bp
* 84182 87362: contig of 3181 bp in length
* 87363 87462: gap of 100 bp
* 87463 91079: contig of 3617 bp in length
* 91080 91179: gap of 100 bp
* 91180 94730: contig of 3551 bp in length
* 94731 94830: gap of 100 bp
* 94831 98146: contig of 3316 bp in length
* 98147 98246: gap of 100 bp
* 98247 102034: contig of 3788 bp in length
* 102035 102134: gap of 100 bp
* 102135 105763: contig of 3629 bp in length
* 105764 105863: gap of 100 bp
* 105864 108749: contig of 2886 bp in length
* 108750 108849: gap of 100 bp
* 108850 113126: contig of 4277 bp in length
* 113127 113226: gap of 100 bp
* 113227 117652: contig of 4426 bp in length
* 117653 117752: gap of 100 bp
* 117753 121602: contig of 3850 bp in length
* 121603 121702: gap of 100 bp
* 121703 126141: contig of 4439 bp in length
* 126142 126241: gap of 100 bp
* 126242 130579: contig of 4338 bp in length
* 130580 130679: gap of 100 bp
* 130680 134477: contig of 3798 bp in length
* 134478 134577: gap of 100 bp
* 134578 141667: contig of 7090 bp in length
* 141668 141767: gap of 100 bp
* 141768 147874: contig of 6107 bp in length
* 147875 147974: gap of 100 bp
* 147975 153773: contig of 5799 bp in length
* 153774 153873: gap of 100 bp
* 153874 160439: contig of 6566 bp in length
* 160440 160539: gap of 100 bp
* 160540 166630: contig of 6091 bp in length
* 166631 166730: gap of 100 bp

```

```

* 166731 174571: contig of 7841 bp in length
* 174572 174671: gap of 100 bp
* 174672 180128: contig of 5457 bp in length
* 180129 180228: gap of 100 bp
* 180229 186362: contig of 6134 bp in length
* 186363 186462: gap of 100 bp
* 186463 193379: contig of 6917 bp in length.
*
FEATURES
  source
    1. .193379
    /organism="Homo sapiens"

```

```

Query Match          3 1%: Score 21; DB 2; Length 193379;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 338 ggcctagagagctgcagagct 358
      |||||||
Db 181205 GGCTAGAGAGAGCTGCAGAGCT 181225

```

```

RESULT 15
RP282365/LOCUS
RP282365 410 bp DNA BCT 07-MAR-1997
DEFINITION
R. prowazekii genomic DNA fragment (clone A336R).
ACCESSION
Z82365
VERSION
Z82365.1 GI:1871716
KEYWORDS
SOURCE
  Rickettsia prowazekii.
  Rickettsia prowazekii.
  Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
  Rickettsiaceae; Rickettsiidae; Rickettsia; typhus group.
  Andersson, S.G., Eriksson, A.S., Naslund, A.K., Andersen, M.S. and
  Kurland, C.G.
  The Rickettsia prowazekii genome: a random sequence analysis
  Microb. Comp. Genomics 1 (4), 293-315 (1996)
  9853639
  2 (bases 1 to 410)
  Andersson, S.G.E.
  Direct Submission
  Submitted (31-OCT-1996) Andersson S.G.E., Department of Molecular
  Biology, Husegatan 3, BOX 590, Biomedical Center, S-751 24
  Uppsala, SWEDEN
  The overall error rate is an estimated 0.5%.
  Location/Qualifiers
    1. .410
    /organism="Rickettsia prowazekii"
    /strain="Madrid E"
    /db_xref="taxon:782"
    /clone_11p="genomic DNA, J. Bacteriol.
    177:4171-4175(1995)"
    /clone="A336R"

```

```

COMMENT
FEATURES
  source
    1. .410
    /organism="Rickettsia prowazekii"
    /strain="Madrid E"
    /db_xref="taxon:782"
    /clone_11p="genomic DNA, J. Bacteriol.
    177:4171-4175(1995)"
    /clone="A336R"

```

```

BASE COUNT      93 a      66 c      84 g      165 t      2 others
ORIGIN

```

```

Query Match          2.9%: Score 20; DB 1; Length 410;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 482 ccacaccttaaatgtgta 501
      |||||||
Db 358 CCACACCTTTAAATTTGTA 339

```

```

Search completed: February 26, 2002, 13:28:46
Job time: 9657 sec

```